



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MSPrch_un n.a. - n.a. database search, using Smith-Waterman algorithm
on: Thu Aug 21 10:07:45 1997: MasPar time 876.69 Seconds
Tabular output not generated. 894.092 Million cell updates/sec

Title: >US-08-469-637A-1
Description: (1-1527) from US08469637A.seq
Perfect Score: 1527
N.A. Sequence: 1 GCGCCAGCGCGCGCTCCAA.....TTCAACTGAGAAAAAAA 1527
Comp: 6CGGGGTGCGCGCGGAGGTT.....AAGTGGACCTTTT

Scoring table:

TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 707517 seqs, 25659390 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

EST-STS
9:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
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45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
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170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

Statistics: Mean 11.463; Variance 1.911; scale 5.997

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	563	36.9	602	195	AA037313	zc52h03.r1 Soares sen	0.00e+00
2	327	21.4	346	73	H88769	YW23g12.r1 Homo sapie	0.00e+00
3	187	12.2	458	49	HUM366H09B	Human aorta CDNA 5'-e	0.00e+00
4	173	11.3	370	49	HUM345E08B	Human aorta CDNA 5'-e	0.00e+00
5	114	7.5	303	49	HUM365F01B	Human aorta CDNA 5'-e	2.56e-195
6	114	7.5	387	49	HUM366H11B	Human aorta CDNA 5'-e	2.56e-195
7	56	3.7	157	140	C02463	HUMGS0012349, Human G	4.02e-65
8	24	1.6	504	5	T72414	yc72a07.r1 Homo sapie	1.55e-06
9	23	1.5	344	61	H14106	ym62a03.r1 Homo sapie	3.63e-05
10	23	1.5	442	5	T71938	ye07c04.r1 Homo sapie	3.63e-05
11	23	1.5	470	2	T60480	yb95d03.s1 Homo sapie	3.63e-05
12	21	1.4	222	53	R94906	Yq39b08.s1 Homo sapie	1.36e-02
13	22	1.4	241	44	H37487	15616 Arabidopsis tha	7.51e-04
14	21	1.4	253	129	HSC08E062	H. sapiens partial cd	1.36e-02
15	22	1.4	267	148	W10583	ma8f10.r1 Soares mou	7.51e-04
16	22	1.4	300	183	AA100384	zn46h08.r1 Strategene	7.51e-04
17	22	1.4	325	19	HUM245F10B	Human aorta CDNA 5'-e	1.36e-02
18	21	1.4	301	65	H29337	ym60h07.s1 Homo sapie	1.36e-02
19	21	1.4	325	112	ATTS3517	A. thaliana transcrib	1.36e-02
20	21	1.4	325	19	T54964	yb42d03.r1 Homo sapie	1.36e-02
21	22	1.4	330	13	R1CC0437A	Rice CDNA, partial se	7.51e-04
22	21	1.4	339	88	H65000	yu66d10.s1 Homo sapie	1.36e-02
23	22	1.4	360	164	C14856	Human fetal brain CDN	7.51e-04
24	21	1.4	362	5	T70903	yc49d03.s1 Homo sapie	1.36e-02
25	21	1.4	380	187	AA142684	mg64e05.r1 Soares 2nb	1.36e-02
26	22	1.4	385	180	AA087288	mo11d06.r1 Life Tech	7.51e-04
27	22	1.4	387	109	H8DH3G03	H. sapiens partial cd	1.36e-02
28	21	1.4	395	5	T71079	yc50c04.r1 Homo sapie	1.36e-02
29	22	1.4	406	126	W76826	me73g11.r1 Soares mou	7.51e-04
30	21	1.4	408	41	R27233	yh53a01.r1 Homo sapie	1.36e-02
31	22	1.4	410	6	T74804	yc66d04.r1 Homo sapie	7.51e-04
32	21	1.4	447	184	AA011021	ze34c01.s1 Soares rec	1.36e-02
33	21	1.4	450	131	N68886	Tg52t3y39d10.r1 Toxop	1.36e-02
34	22	1.4	453	193	AA164719	zo93f04.s1 Strategene	7.51e-04
35	22	1.4	453	111	N21157	yx47d01.s1 Homo sapie	7.51e-04
36	21	1.4	465	193	AA164056	mt67g06.r1 Soares mou	1.36e-02
37	22	1.4	465	5	T77351	yd7ze10.r1 Homo sapie	7.51e-04
38	22	1.4	472	57	T42477	5740 Arabidopsis thal	7.51e-04
39	21	1.4	472	147	AA003244	mg48g01.r1 Soares mou	1.36e-02
40	21	1.4	478	177	AA061066	mj66h11.r1 Soares mou	1.36e-02
41	21	1.4	493	15	W81931	me33c11.r1 Soares mou	1.36e-02
42	22	1.4	480	55	R1CS1559A	Rice CDNA, partial se	7.51e-04
43	21	1.4	500	94	N38845	YH80d11.s1 Homo sapie	1.36e-02
44	22	1.4	506	117	W29026	55c10 Human retina CD	7.51e-04
45	21	1.4	798	115	W22001	62e8 Human retina CDN	1.36e-02

ALIGNMENTS

RESULT 1
LOCUS AA037313 602 bp mRNA EST 25-NOV-1996
DEFINITION zc52h03.r1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA
ACCESSION AA037313
NID clone 325973 5'
KEYWORDS g1512420
EST.

SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 602)
 Hillier, L., Clark, N., Dubnue, T., Ellston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Ratkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevisakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 COMMENT
 TITLE
 JOURNAL
 CONTACT: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 TEL: 314 286 1800
 FAX: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1203 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 435.

FEATURES
source

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/organism="Homo sapiens"
/notc="Vector: pT73D (Pharmacia) with a modified
polylinker V.Type: phagemid; Site_1: Not I; Site_2: Eco
RI; TGTACCATCTGAAATGAGGACCGCCGATTTTTTTTTTTTTT
3'1, double-stranded cDNA was site selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bentic
Soares and M.Fatima Bonaldo."
/clone="325973"
/clone_1lb="Soares senescent fibroblasts NbHsp"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
<1..>602
MRNA
BASE COUNT      209 a      128 c      136 g      126 t      3 others
ORIGIN

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Query Match	36.9%;	Score 563;	DB 195;	Length 602;
Best Local Similarity	98.7%;	Pred. No. 0.00e+00;		
Matches	588;	Conservative	0;	Mismatches 4; Indels 4; Gaps 4

[illegible]

Db	362	ccttctggaataaacgcttgtagcgagacatcttggaacatctaaacctcaactttagaacagc	421
Oy	870	cctctctgtaaaaacgctctgtagcgggacacatcttg- acatctgaacctctacaccttgacacac	928
Db	422	ttctctgtagctgtagtgaataagcttaccgsggaataaagttgtagcagaagaacttgtaaaa	481
Oy	929	tt- cgtagcttgtagtgaataagcttaccgsggaataaagttgtagcagaagaacttgtaaaa	987
Db	482	acataataagcattgcataaaccccaagtgcacagatctctgaagctgtcagttcttggcgata	541
Oy	988	acataataagcattgcataaaccccaagtcacagacacacatctgaagctgtcagttcttggcgata	104
Db	542	aaaatctgcagcagaaganaacctctgaaaggginctaagcaacgacttaagcatca	597
Oy	1048	aaaatctgcagcagaagacacactcttgaa- gggccttaatgcacgacttaaaagcactca	1102

LOCUS	2	H88769	346 bp	mRNA	EST	22-NOV-1999
DEFINITION		YW2312.r1	Homo sapiens cDNA clone 253126.5.			
ACCESSION		H88769				
NID		61071029				
KEYWORDS		EST.				
SOURCE		human clone=253126	primer=M13RP1	library=Morton	Fetal Cochlea	

ORGANISM

REFERENCE
HALLER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,
1 (bases 1 to 346)
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Celemata;
Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 346)

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

	Contact: Wilson RK WashU-Merck ESP Project Washington University School of Medicine 4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
	Tel.: 314 286 1800 Fax: 314 286 1810 Email: estewartson.wustl.edu
	High quality sequence stops: 278
	Source: IMAGE Consortium, LIND
	This clone is available royalty-free through LIND ; contact the IMAGE Consortium (info@image.lind.gov) for further information.
FEATURES	
SOURCE	location/Qualifiers
	1..346
	/organism="Homo sapiens"
	/clone="Z53I26"
MRNA	<1..>346
BASE COUNT	104 a 71 c 62 g 106 t 3 others
ORIGIN	

	Query Match	21.4%	Score 327	DB 73	Length 346
Best Local Similarity	98.3%		Pred. 0.00e+00		
Matches 340	Conservative	0	Mismatches 4	Indels 2	Gaps 2
Db	1	tcaggttccttcacaggttcacatgacacaaatggttcacgaagtatttttagaata	60		
QY	1151	TCAGGTTCTTCACAGGCTTCACAAATGTAACAATTTGTAACGAACTTTTAA	1210		
Db	61	taggttaaccaggttcacatcagcattaanaataagctctcttaactgaatgacattagc	120		
QY	1211	TAGGTAAACCAAGTCCAAACAGTATAAAATTAAGCTCTCTTAATCTGGAATGGCCATTGAGC	1270		

DB	121	tgctccccaacattggcagagatccccaatgagatgaagaaactgtttctcaggagactggg	180							
QY	1271	TGTTTCTCCACAAATGGCGAGATCCATGGATGATGAAGTATGTTTCTCAGGACTTGGAG	1330							
Db	181	cttcacgtgatatactttctcattaccacagttactaatlttggccacaggyacttaagaagaa	240							
QY	1331	CTTTCAGAGATATCTTCTCATTTACCGAGTACTAATATTGGCCACAGGATACATAAAGAA	1390							
Db	241	ctatgagtgtgagaagagactaacatctctccataaaccacaatggttaatccaac	300							
QY	1391	CTAAGATGTGGAGAAAGAACTAATATCTCTCCAAATAAACCCCAATGGTT-ATATCAAC	1449							
Db	301	tgtagacttgagctgtatcactactactgagactatgtttcccccintta	346							
QY	1450	TGTGATGATCTGGATCTGATTACTACTG-ACATATATTTTCCCTTATTA	1494							
RESULT	3	HUM366H09B	458 bp	MRNA	EST	29-AUG-1995				
DESCRIPTION		Human aorta cDNA 5'-end	GEN-366H09.							
ACCESSION		D63125								
NID		9368050								
KEYWORDS		EST (expressed sequence tag); Human aorta; similar to none (May 29, 1995).								
SOURCE		Human sapiens (library: Clontech human aorta polyA+ mRNA (#572))								
ORGANISM		Human sapiens								
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 458)								
AUTHORS		Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimoda,Y., Shinomiya,H., Takaiuchi,A., Takeda,S., Matenabe,T., Takahashi,E.-I., Hirai,Y., Mekawa,H., Shin,S. and Nakamura,Y.								
TITLE		Unpublished (303)								
JOURNAL		Unpublished (1995)								
COMMENT		Submitted (30-May-1995) to DDBJ by: Tsutomu Fujiwara								
		Otsuka GEN Research Institute								
		Otsuka Pharmaceutical Co., Ltd								
		463-10 Kagasuno Kawachi-cho								
		Tokushima, Tokushima								
		771-01								
		Japan								
		Phone: 0886-65-2888								
		Fax : 0886-37-1035.								
BASE COUNT		157 a	74 c	66 g	161 t					
ORIGIN		Location/Qualifiers								
		1..458	/organism="Homo sapiens"							
		/clone.lib="Clontech human aorta polyA+ mRNA (#572)"								
FEATURES		source								
Query Match		12.2%;	Score 187;	DB 49;	Length 458;					
Best Local Similarity		99.0%;	Pred. No. 0.0e+00;							
Matches 189;		Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;				
Db	1	gtgatatctttctcattaccacagtgactaatlttggccacaggggtactcaagaactatga	60							
QY	1337	GTGATATCTTCTCATATTACCAAGTACATAATTTGGCCACAGGGTACTAAAAAGAAACTATGA	1396							
Db	61	tgtagagaaagagactaacatctctcccaataaaccacaatggttaatccaactgcaga	120							
QY	1397	TGTGAGAAAGAGATACATCTCTCTCCAAATAAACCCCAATGGTTATATCCAACTGTGAGA	1456							
Db	121	tctgagatcgtatctactgactatctatattttcccttattactgcttgcagtaattcaactgy	180							
QY	1457	TCTGATGATCTGATCTACTGACTATATTTTCCCTTATTACTGCTTGCAAGTAATTCAACTGG	1516							
Db	181	aatataaaaaa	191							
QY	1517	AAAAAAAAAAAA	1527							

RESULT	4	HUM345E08B	370 bp	MRNA	EST	29-AUG-1995
LOCUS		Human aorta cDNA 5'-end	GEN=345E08.			
DEFINITION		Human aorta cDNA 5'-end	GEN=345E08.			
ACCESSION		D62967				
KEYWORDS		EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).				
SOURCE		Human sapiens (library: Clontech human aorta polyA+ mRNA (#5572))				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS		1 (bases 1 to 370) Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takachi,A., Takeda,S., Matsumae,T., Takahashi,E.-I., Hirai,Y., Makawa,H., Shin,S. and Nakamura,Y.				
TITLE		Unpublished(303)				
JOURNAL		Unpublished(303)				
COMMENT		Submitted (30-May-1995) to DDBJ by: Automu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 Kagasuno Kawachi-cho Tokushima, Tokushima 771-01 Japan Phone: 0886-65-2888 Fax : 0886-37-1035.				
FEATURES		Location/Qualifiers				
SOURCE		1..370 /organism="Homo sapiens" /clone_lib="Clontech human aorta polyA+ mRNA (#572)"				
BASE COUNT		122 a 63 c 55 g 127 t				3 others
ORIGIN						
Query Match		11.3%; Score 173; DB 49; Length 370;				
Best Local Similarity		97.9%; Pred. No. 0.00e+00;				
Matches 187; Conservative		0; Mismatches 2; Indels 2; Gaps 2;				
Db	1	gtgatcatttcctattaccagcagcactaatttgcacagggctacaaagaactatga	60			
QY	1337	GTGATACCTTTCATCAATCCAGTACATATTGCGCACAGGGTACTAAAGAACTATCA	1396			
Db	61	tgttgagaaaggactaacatctccccaataaaccccaaatggttaatccaactgcaga	120			
QY	1397	TGTGAGAAAGGACTAATCAATCTCTCCAAATAAACCCCAATGGTTATATCCAACTGCAGA	1456			
Db	121	t-tggatcgttattctactgactatatttcc-ttattactgcttcagtaattcaactg	178			
QY	1457	TCTGATCGTATCTACTGACTATATTTCCTTATTACTGCTTGCAGTAATTCACATCG	1516			
Db	179	aaatataaaa 189				
QY	1517	AAAAAAAAAAAA 1527				
RESULT	5					
LOCUS		HUM365F01B	303 bp	MRNA	EST	29-AUG-1995
DEFINITION		Human aorta cDNA 5'-end	GEN=365F01.			
ACCESSION		D63118				
KEYWORDS		EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).				
SOURCE		Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS		1 (bases 1 to 303) Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,				

Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takachi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,
Mekawa, H., Shin, S. and Nakamura, Y.
Unpublished (303)
Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers

FEATURES
Source

1..303
/organism="Homo sapiens"

COUNT 102 a 54 c 37 g 106 t 4 others
/clone.lib="Clontech human aorta polyA+ mRNA (#6572)"

Query Match 7.5%; Score 114; DB 49; Length 303;
Best Local Similarity 98.3%; Pred. No. 2,566-195;
Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctaccatctctccaataaaccgaatggtatccacgtcagatcgtat 60
|||
QY 1410 CTACACCTCTCCCAATAAACCCCAAGGTATCCACAGTCAGATCGATGAT 1469
|||
QY 1470 CTACTGACTATATTTCCCTTATCTCTGACGATTAACCTGAAAAA 1527
|||

RESULT 6
LOCUS HUM366H1B 387 bp mRNA EST 29-AUG-1995
DEFINITION Human aorta cDNA 5'-end GEN-566H1.
ACCESSION D63126
NID 9686051
KEYWORDS EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).
SOURCE Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 387)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takachi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,
Mekawa, H., Shin, S. and Nakamura, Y.
Unpublished (303)
Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers

FEATURES

Source 1..387
/organism="Homo sapiens"

COUNT 135 a 62 c 50 g 140 t
/clone.lib="Clontech human aorta polyA+ mRNA (#6572)"

Query Match 7.5%; Score 114; DB 49; Length 387;
Best Local Similarity 98.3%; Pred. No. 2,566-195;

Db 1 ctaccatctctccaataaaccgaatggtatccacgtcagatcgtat 60
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QY 1410 CTACACCTCTCCCAATAAACCCCAAGGTATCCACAGTCAGATCGATGAT 1469
|||
QY 1470 CTACTGACTATATTTCCCTTATCTCTGACGATTAACCTGAAAAA 1527
|||

RESULT 8
LOCUS T72414 504 bp mRNA EST 01-MAR-1995
DEFINITION YC72407 r1 Homo sapiens cDNA clone 86196 5' similar to
gD:X54486_fnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);
ACCESSION T72414
NID 9686935
KEYWORDS EST.
SOURCE human clone=86196 library=Stratagene liver (#937224)
vector=pbuescript SK host=SOB cells (kanamycin resistant)
primer-M13P1 Rsite1-EcoRI Rsite2-XhoI Cloned unidirectionally.
Primer: Oligo dT. Hepatectomy from normal 49 year old male
caucasian. Average insert size: 1.1 kb; Uni-TAP XR Vector; 5'
adaptor sequence: 5'-GAATTCGCGACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTCTTTTCTTTT-3'.

Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctaccatctctccaataaaccgaatggtatccacgtcagatcgtat 60
|||
QY 1410 CTACACCTCTCCCAATAAACCCCAAGGTATCCACAGTCAGATCGATGAT 1469
|||
Db 61 ctactgactatattcccttactactgcttcgagtaattcaactggaattaaaaa 118
|||
QY 1470 CTACTGACTATATTTCCCTTATCTCTGACGATTAACCTGAAAAA 1527
|||

RESULT 7
LOCUS C02463 157 bp DNA EST 11-JUL-1996
DEFINITION HUMS0012349, Human gene signature, 3'-directed cDNA sequence.
ACCESSION C02463
NID 91434693
KEYWORDS gene signature; GS: EST(expressed sequence tag); BodyMap; gene
expression.
SOURCE One or more human adult tissue.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 157)
Direct Submission
Submitted (28-DEC-1995) to the DDBJ/EMBL/GenBank databases. Kousaku
Okubo, Osaka University, Institute for Molecular and Cellular Bio;
1-3, Yamada-Oka, Suita, Osaka Pref. 565, Japan
(E-mail:kousaku@imcb.osaka-u.ac.jp, Tel:06-877-5111(ex.3315),
Fax:06-877-1922)
2 (bases 1 to 157)
Okubo, K.
BodyMap: human gene expression database
Unpublished (1995)
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
Location/Qualifiers

Source 1..157
/organism="Homo sapiens"

COUNT 46 a 26 c 24 g 54 t 7 others

Query Match 3.7%; Score 56; DB 140; Length 157;
Best Local Similarity 95.5%; Pred. No. 4,026-65;
Matches 64; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 1 gatcgtactactgactatattcccttactactgcttcgagtaattcaactgga 60
|||
QY 1461 GATCGTATCTACTGACTATATTTCCCT-TATTACTGCTTGCAAGTAATCACTGAAA 1519
|||

Db 61 ttaaaaa 67
|||
QY 1520 AAAAAA 1526

RESULT 8
LOCUS T72414 504 bp mRNA EST 01-MAR-1995
DEFINITION YC72407 r1 Homo sapiens cDNA clone 86196 5' similar to
gD:X54486_fnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);
ACCESSION T72414
NID 9686935
KEYWORDS EST.
SOURCE human clone=86196 library=Stratagene liver (#937224)
vector=pbuescript SK host=SOB cells (kanamycin resistant)
primer-M13P1 Rsite1-EcoRI Rsite2-XhoI Cloned unidirectionally.
Primer: Oligo dT. Hepatectomy from normal 49 year old male
caucasian. Average insert size: 1.1 kb; Uni-TAP XR Vector; 5'
adaptor sequence: 5'-GAATTCGCGACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTCTTTTCTTTT-3'.

ORIGIN

Query Match 1.5%; Score 23; DB 5; Length 442;

Best Local Similarity 79.5%; Pred. No. 3.63e-05;

Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 332 agcacatgggaacagggttccaggccctctctgtttt 370

Cp 1022 AGGATCTGCTCAGTGGTTTCATGCTTATTTGTTT 984

RESULT 11

LOCUS T60480 470 bp mRNA EST 13-FEB-1995

DEFINITION yb55d03.s1 Homo sapiens cDNA clone 78917 3' similar to gb:X04225

ALPHA-1-MICROGLOBULIN (HUMAN);

ACCESSION T60480

NID 9663517

KEYWORDS EST.

SOURCE human clone-78917 library-stratagene liver (#937224)

vector-pbluescript SK host-SOBR cells (kanamycin resistant)

primer-21m3 RstI-EcoRI RstI-EcoRI cloned unidirectionally.

primer: oligo dt Hepatectomy from normal 49 year old male

caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5'

adaptor sequence: 5'-GAATTCGGCAG-3'; 3' adaptor sequence:

5'-CTCGAGTCTTTTCTTTTCTTTTCTTTT-3'.

ORGANISM Homo sapiens

Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 470)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaekis,E.,

Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

Washu-Merck EST Project

Unpublished (1995)

TITLE Contact: Wilson RK

JOURNAL Washu-Merck EST Project

COMMENT Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 374

Source: IMAGE Consortium, LNL.

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES Location/Qualifiers

source 1..470

BASE COUNT 95 a 137 c 125 g 108 t 5 others

ORIGIN /organism="Homo sapiens"

/clone="78917"

Query Match 1.5%; Score 23; DB 2; Length 470;

Best Local Similarity 72.3%; Pred. No. 3.63e-05;

Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 407 ccatggatgtaccatttttaggaataaccgtgctgcatcc 453

Cp 1300 CCATGGATGTCCCAATGTGAGGAACACGCTCATGCGCATTTCC 1254

RESULT 12

LOCUS R94906 222 bp mRNA EST 31-AUG-1995

DEFINITION y939b08.s1 Homo sapiens cDNA clone 198135 3'.

ACCESSION R94906

NID 9973636

KEYWORDS EST.

SOURCE human clone-198135 primer-Promega -21m3 library-Soares fetal liver

spleen INRIS vector-pT713D (Pharmacia) with a modified polylinker

host-pH10B (ampicillin resistant) RstI-Eco I RstI-Eco RI liver

and spleen from a 20 week-post conception male fetus. 1st strand

cDNA was primed with a Pac I - oligo(dt) primer [5' AACTGAGAGATTAATTAAGACATTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patrina Bonaldi.

ORGANISM

Homo sapiens

Eucaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 222)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

Washu-Merck EST Project

Unpublished (1995)

TITLE Contact: Wilson RK

JOURNAL Washu-Merck EST Project

COMMENT Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 201

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES Location/Qualifiers

source 1..222

BASE COUNT 31 a 84 c 1 g 77 t 29 others

ORIGIN /organism="Homo sapiens"

/clone="198135"

<1..>222

Query Match 1.4%; Score 21; DB 53; Length 222;

Best Local Similarity 60.0%; Pred. No. 1.36e-02;

Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 131 tttcttntttnaattcttcttcttcaattcttcaacnaaatccatc 185

Cp 994 TTATGTTTTCATGCTTCTGCTCCCATTTCTTCCGGTAAGCTTCCAT 940

RESULT 13

LOCUS H37487 241 bp mRNA EST 25-JUL-1995

DEFINITION 15616 Arabidopsis thaliana cDNA clone 182E107.

ACCESSION H37487

NID 9906986

KEYWORDS EST.

SOURCE the cress clone-182E107 library-lambda-PR2 strain-var columbia

vector-lambda zip-lox primer-T7 dye primer RstI-EcoRI Sal RstI-EcoRI

lambda PR2 is a cDNA library derived from equal quantities of 4

pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated

seedlings; 2) tissue culture grown roots; 3) staged plants half

with 24 hour light cycle, half on 16 hr light, 8 hour dark-

rosettes; 4) same plants as 3 but aerial tissue (stems, flowers

and siliques. The vector is BRL's lambda zip-lox. The cDNA

inserts were directionally cloned with Sal-Not arms using oligo dt

primed cDNA.

ORGANISM Arabidopsis thaliana

Eucaryotes; Embryophyta; Magnoliophyta; Magnoliopsida; Capareales;

Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 241)

Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,

McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,

Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Journal Comment

Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22j13cne@bm.cl.msu.edu.

Location/Qualifiers

1..241
/organism="Arabidopsis thaliana"
/clone="182E107"
/strain="var Columbia"

BASE COUNT 72 a 41 c 50 g 70 t 8 others

ORIGIN

Query Match 1.4%; Score 22; DB 44; Length 241;
Best Local Similarity 74.4%; Pred. No. 7.51e+04;
Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Dp 32 aaaataatcagaagaagatcatcgatgcgatattgtat 74
||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1485 AAAATATGTCAGTACGTACCATCTCACATCTGCACATTGGAT 1443

RESULT 14 HSCOE062 253 bp RNA EST 21-SEP-1995
LOCUS H.sapiens partial CDNA sequence; clone c-Obse06.
DEFINITION J28433
ACCESSION 9360441
MID partial CDNA sequence; transcribed sequence fragment.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 253)
AUTHORS Genexpress.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France
and Genetique Molculaire et Biologie du developpement, CNRS UPR422
B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
2 (bases 1 to 253)
Genexpress.
The Genexpress CDNA program
unpublished
3 (bases 1 to 253)
Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C.,
Doreigne,M.D., Duprat,S., Houligatte,R., Juneau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pletiot,G., Pouillot,Y.,
Sebastien-Kabarkchts,C. and Tessier,A.
IMGE: molecular integration of the analysis of the human genome
and its expression
C.R.Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
Clone library from B.Souares, Psychiatry Dept. Columbia University
USA.

JOURNAL MEDLINE
COMMENT

TITLE
JOURNAL
MEDLINE
COMMENT

No significant homology found with :
genbank release 81 swissprot release 28.
Location/Qualifiers

```

SOURCE
1..253
/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"

BASE COUNT      76 a       57 c       49 g       70 t       1 others
ORIGIN

Query Match          1.4%   Score 21; DB 129; Length 253;
Best Local Similarity 78.4%; Pred No. 1,36e-02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db    123 acacagctcacatgttacagacaataaacgtcgaag 159
      ||||| | | | | | | | | | | | | | | | | |
Oy    774 ACACAGCTCACACAGACAGACTTCCACCCTCCTGAG 810

RESULT 15
LOCUS     W10583           267 bp      mRNA                      EST              05-SEP-1996
DEFINITION mas8f10.r1 Soares mouse pJNMF19.5 Mus musculus cDNA clone 313003 5'
            similar to gb:219554 VIMENTIN (HUMAN)).
ACCESSION W10583
MID        91284900
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.
REFERENCE 1 (bases 1 to 267)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Putative full length read
            Seq primer: EMPprimer.
            Location/Qualifiers
                1..267
                    /organism="Mus musculus"
                    /note="Vector: pUT3D (Pharmacia) with a modified
                    polylinker; Site.1: Not I - Eco RI; 1st strand cDNA
                    was primed with a Not I - oligo(dT) primer [5',
                    TGTTACCAATCTGAAGCGGAGGGCGGCATTTTTTTTTTTTTTTT 3'],
                    double-stranded cDNA was size selected, ligated to Eco RI
                    adapters (Pharmacia), digested with Not I and cloned into
                    the Not I and Eco RI sites of a modified pUT3 vector
                    (Pharmacia). Library went through one round of
                    normalization to a Cot = 5 library constructed by Bento
                    Soares and M.Fatima Bonaldo. RNA was kindly provided by
                    Dr. Minoru Ko (Wayne State University)."
                    /clone="313003"
                    /clone_lib="Soares mouse pJNMF19.5"
                    /dev_stage="19.5 dpc total fetus"
                    /lab_host="DH10B (ampicillin resistant)"
                    <1..>267

BASE COUNT      78 a       70 c       61 g       58 t
ORIGIN

```

Query Match 1.4%; Score 22; DB 148; Length 267;
 Best Local Similarity 75.0%; Pred. No. 7.51e-04;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Db 31 gaagctgctggaagcgagagacatgattctctgctctgc 74
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 931 GAAGCTGCTCGAAGTGAGGTAGCATGTCCAAATGTGCGCTGC 888

Search completed: Thu Aug 21 10:35:06 1997
 Job time : 1641 secs.